

00 0520 250  
00 0520 250

SEQUENCE LISTING

5 <110> Michel, Albrecht  
Scheffler, Brian E.  
Netherland, Michael D.  
Dayan, Franck E.  
Arias de Ares, Renee S.

10 <120> HERBICIDE-RESISTANT PLANTS, AND POLYNUCLEOTIDES AND  
METHODS FOR PROVIDING SAME

<130>

15 <140>  
<141>

<160> 8

20 <170> PatentIn Ver. 2.1

<210> 1  
<211> 1982  
<212> DNA

25 <213> Hydrilla verticillata

<220>  
<221> CDS  
<222> (6)..(1748)

30 <400> 1  
caaac atg act gtt gct agg tcg gtc gtt gca gtc aat cta agt ggt tcc  
50  
Met Thr Val Ala Arg Ser Val Val Ala Val Asn Leu Ser Gly Ser  
35 1 5 10 15

ctt caa aac aga tac cca gcc agt tca tca gtc agc tgc ttc ctt ggc  
98  
Leu Gln Asn Arg Tyr Pro Ala Ser Ser Ser Val Ser Cys Phe Leu Gly  
40 20 25 30

aaa gag tac aga tgc aac agt atg tta gga ttc tgc ggt agt gga aaa  
146  
Lys Glu Tyr Arg Cys Asn Ser Met Leu Gly Phe Cys Gly Ser Gly Lys  
45 35 40 45

ttg gct ttt ggc gca aat gca ccc tat tct aag att gca gct acc aaa  
194  
Leu Ala Phe Gly Ala Asn Ala Pro Tyr Ser Lys Ile Ala Ala Thr Lys  
50 50 55 60

cca aag ccc aaa ctt cgc cct ttg aag gtc aac tgc atg gat ttc cca  
242  
Pro Lys Pro Lys Leu Arg Pro Leu Lys Val Asn Cys Met Asp Phe Pro  
55 65 70 75

aga cct gat ata gat aac act gct aat ttc ttg gaa gct gct gct ctt  
 290  
 5 Arg Pro Asp Ile Asp Asn Thr Ala Asn Phe Leu Glu Ala Ala Ala Leu  
 80 85 90 95

tct tcc tct ttt cgc aat tca gca aga cca agt aaa cct ctt caa gtt  
 338  
 10 Ser Ser Ser Phe Arg Asn Ser Ala Arg Pro Ser Lys Pro Leu Gln Val  
 100 105 110

gta att gct ggt gca ggt ttg gct ggt ctt tca aca gca aag tat ctc  
 386  
 15 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu  
 115 120 125

gca gat gca ggg cac ata ccc ata cta ctg gag gct aga gat gta ttg  
 434  
 20 Ala Asp Ala Gly His Ile Pro Ile Leu Leu Glu Ala Arg Asp Val Leu  
 130 135 140

ggt ggc aag gtg gca gcg tgg aaa gat gat gat gga gac tgg tat gag  
 482  
 25 Gly Gly Lys Val Ala Ala Trp Lys Asp Asp Asp Gly Asp Trp Tyr Glu  
 145 150 155

aca ggc ctg cat ata ttt ttt ggt gca tat ccc aat gtg cag aat tta  
 530  
 30 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Val Gln Asn Leu  
 160 165 170 175

ttt ggt gaa ctt ggc ata aat gat cgt cta caa tgg aaa gag cat tca  
 578  
 35 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser  
 180 185 190

atg att ttt gcg atg cca aac aag cca ggg gaa ttt agt cgc ttt gat  
 626  
 40 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp  
 195 200 205

ttt cca gaa gta ctt cct gct cca cta aat gga ata tgg gca atc ctt  
 674  
 45 Phe Pro Glu Val Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu  
 210 215 220

aaa aac aat gaa atg ctc act tgg cca gag aaa gtg caa ttt gct att  
 722  
 50 Lys Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Gln Phe Ala Ile  
 225 230 235

gga cta cta cct gca atg att ggg ggg cag cca tat gtt gaa gct cag  
 770  
 55 Gly Leu Leu Pro Ala Met Ile Gly Gly Gln Pro Tyr Val Glu Ala Gln  
 240 245 250 255

gat ggc tta aca gtt caa gag tgg atg aga aaa cag ggt gtg ccg gat  
 818  
 5 Asp Gly Leu Thr Val Gln Glu Trp Met Arg Lys Gln Gly Val Pro Asp  
 260 265 270

cga gtc aat gac gag gtt ttc att gca atg tca aag gct ctt aac ttc  
 866  
 10 Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe  
 275 280 285

ata aac cct gat gaa ctt tcc atg caa tgc atc ctg att gcc tta aac  
 914  
 15 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn  
 290 295 300

cgt ttc ctt cag gaa aag cat ggg tgc aag atg gcc ttt tta gat ggt  
 962  
 20 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly  
 305 310 315

aat cca cct gaa aga tta tgt aag cca att gct gat cac atc gag tca  
 1010  
 25 Asn Pro Pro Glu Arg Leu Cys Lys Pro Ile Ala Asp His Ile Glu Ser  
 320 325 330 335

ttg ggt ggc caa gtc atc ctt aat tcc cga ata cag aag att gag ctg  
 1058  
 30 Leu Gly Gly Gln Val Ile Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu  
 340 345 350

aat gca gac aaa tcc gtc aag cat ttt gtg ctc acc aat gga aat ata  
 1106  
 35 Asn Ala Asp Lys Ser Val Lys His Phe Val Leu Thr Asn Gly Asn Ile  
 355 360 365

ata aca gga gat gca tat gta ttt gca aca cct gtt gat atc ttg aag  
 1154  
 40 Ile Thr Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys  
 370 375 380

ctt ctg tta cct gaa gat tgg aag gag att tca tat ttc aaa aaa ttg  
 1202  
 45 Leu Leu Leu Pro Glu Asp Trp Lys Glu Ile Ser Tyr Phe Lys Lys Leu  
 385 390 395

gac aag ttg gtt ggc gta cct gtg ata aat gta cac ata tgg ttt gat  
 1250  
 50 Asp Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp  
 400 405 410 415

agg aag ttg aag aac aca tac gat cat ctt ctt ttc agc agg agt cca  
 1298  
 55 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro  
 420 425 430

ctg ttg agc gtt tat gca gac atg tct gtt aca tgc aag gaa tac tac  
 1346  
 5 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr  
 435 440 445

aat cca aat caa tcc atg ctt gag cta gta ttt gca cca gca gag aaa  
 1394  
 10 Asn Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Lys  
 450 455 460

tgg att tca tgc agt gac agt gaa atc att aac gcg act atg caa gag  
 1442  
 15 Trp Ile Ser Cys Ser Asp Ser Glu Ile Ile Asn Ala Thr Met Gln Glu  
 465 470 475

ctt gct aaa ctc ttt cca gat gag att tct gct gat caa agc aag gcc  
 1490  
 20 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala  
 480 485 490 495

aaa att ttg aaa tat cat gtt gta aag acc ccg agg tca gtt tac aag  
 1538  
 25 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys  
 500 505 510

acg gtc cct gat tgt gaa cca tgc cgg cct ttg caa aga tct cca att  
 1586  
 30 Thr Val Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile  
 515 520 525

gaa ggg ttc tac ttg gct ggt gac tac aca aag cag aag tat ttg gcc  
 1634  
 35 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala  
 530 535 540

tca atg gaa ggt gcc gtg tta tct ggg aag cta tgt gct cag gca att  
 1682  
 40 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile  
 545 550 555

gtg cag gac tgc agc ttg ttg gct tct agg gta cag aaa agc cca cag  
 1730  
 45 Val Gln Asp Cys Ser Leu Leu Ala Ser Arg Val Gln Lys Ser Pro Gln  
 560 565 570 575

acg ttg acg att gcc tga ttcaggaaac ttttatgcag gttcagtttg  
 1778  
 50 Thr Leu Thr Ile Ala  
 580

tagggggaat atttctgggt ttgtttcatt cagatgtttt tcttttagag catatgtctt  
 1838

55 tatagtaaaa actcccacct ctttctcatg tatagctaca tcagcaagca aaggggggtaa  
 1898

gttgcaattt caggacttga acatggcctc tgcacaggta aagacagaat ggacataaat  
1958

5 gcaagcatgg aatttacaat attc  
1982

10 <210> 2  
<211> 580  
<212> PRT  
<213> Hydrilla verticillata

<400> 2

15	Met	Thr	Val	Ala	Arg	Ser	Val	Val	Ala	Val	Asn	Leu	Ser	Gly	Ser	Leu
	1				5					10					15	
	Gln	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Ser	Val	Ser	Cys	Phe	Leu	Gly	Lys
				20					25					30		
	Glu	Tyr	Arg	Cys	Asn	Ser	Met	Leu	Gly	Phe	Cys	Gly	Ser	Gly	Lys	Leu
20			35					40					45			
	Ala	Phe	Gly	Ala	Asn	Ala	Pro	Tyr	Ser	Lys	Ile	Ala	Ala	Thr	Lys	Pro
		50					55					60				
	Lys	Pro	Lys	Leu	Arg	Pro	Leu	Lys	Val	Asn	Cys	Met	Asp	Phe	Pro	Arg
	65					70					75					80
25	Pro	Asp	Ile	Asp	Asn	Thr	Ala	Asn	Phe	Leu	Glu	Ala	Ala	Ala	Leu	Ser
					85					90					95	
	Ser	Ser	Phe	Arg	Asn	Ser	Ala	Arg	Pro	Ser	Lys	Pro	Leu	Gln	Val	Val
				100					105					110		
	Ile	Ala	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Ser	Thr	Ala	Lys	Tyr	Leu	Ala
30			115					120					125			
	Asp	Ala	Gly	His	Ile	Pro	Ile	Leu	Leu	Glu	Ala	Arg	Asp	Val	Leu	Gly
		130					135					140				
	Gly	Lys	Val	Ala	Ala	Trp	Lys	Asp	Asp	Asp	Gly	Asp	Trp	Tyr	Glu	Thr
	145					150					155					160
35	Gly	Leu	His	Ile	Phe	Phe	Gly	Ala	Tyr	Pro	Asn	Val	Gln	Asn	Leu	Phe
					165					170					175	
	Gly	Glu	Leu	Gly	Ile	Asn	Asp	Arg	Leu	Gln	Trp	Lys	Glu	His	Ser	Met
				180					185					190		
	Ile	Phe	Ala	Met	Pro	Asn	Lys	Pro	Gly	Glu	Phe	Ser	Arg	Phe	Asp	Phe
40			195						200					205		
	Pro	Glu	Val	Leu	Pro	Ala	Pro	Leu	Asn	Gly	Ile	Trp	Ala	Ile	Leu	Lys
		210					215						220			
	Asn	Asn	Glu	Met	Leu	Thr	Trp	Pro	Glu	Lys	Val	Gln	Phe	Ala	Ile	Gly
	225					230					235					240
45	Leu	Leu	Pro	Ala	Met	Ile	Gly	Gly	Gln	Pro	Tyr	Val	Glu	Ala	Gln	Asp
					245					250					255	
	Gly	Leu	Thr	Val	Gln	Glu	Trp	Met	Arg	Lys	Gln	Gly	Val	Pro	Asp	Arg
				260					265					270		
	Val	Asn	Asp	Glu	Val	Phe	Ile	Ala	Met	Ser	Lys	Ala	Leu	Asn	Phe	Ile
50			275					280						285		
	Asn	Pro	Asp	Glu	Leu	Ser	Met	Gln	Cys	Ile	Leu	Ile	Ala	Leu	Asn	Arg
		290					295					300				
	Phe	Leu	Gln	Glu	Lys	His	Gly	Ser	Lys	Met	Ala	Phe	Leu	Asp	Gly	Asn
	305					310					315					320
55	Pro	Pro	Glu	Arg	Leu	Cys	Lys	Pro	Ile	Ala	Asp	His	Ile	Glu	Ser	Leu
					325					330				335		
	Gly	Gly	Gln	Val	Ile	Leu	Asn	Ser	Arg	Ile	Gln	Lys	Ile	Glu	Leu	Asn

				340					345				350			
	Ala	Asp	Lys	Ser	Val	Lys	His	Phe	Val	Leu	Thr	Asn	Gly	Asn	Ile	Ile
			355					360					365			
5	Thr	Gly	Asp	Ala	Tyr	Val	Phe	Ala	Thr	Pro	Val	Asp	Ile	Leu	Lys	Leu
		370					375					380				
	Leu	Leu	Pro	Glu	Asp	Trp	Lys	Glu	Ile	Ser	Tyr	Phe	Lys	Lys	Leu	Asp
	385					390					395					400
	Lys	Leu	Val	Gly	Val	Pro	Val	Ile	Asn	Val	His	Ile	Trp	Phe	Asp	Arg
				405						410					415	
10	Lys	Leu	Lys	Asn	Thr	Tyr	Asp	His	Leu	Leu	Phe	Ser	Arg	Ser	Pro	Leu
			420						425					430		
	Leu	Ser	Val	Tyr	Ala	Asp	Met	Ser	Val	Thr	Cys	Lys	Glu	Tyr	Tyr	Asn
		435						440					445			
	Pro	Asn	Gln	Ser	Met	Leu	Glu	Leu	Val	Phe	Ala	Pro	Ala	Glu	Lys	Trp
15		450					455					460				
	Ile	Ser	Cys	Ser	Asp	Ser	Glu	Ile	Ile	Asn	Ala	Thr	Met	Gln	Glu	Leu
	465					470				475						480
	Ala	Lys	Leu	Phe	Pro	Asp	Glu	Ile	Ser	Ala	Asp	Gln	Ser	Lys	Ala	Lys
				485					490						495	
20	Ile	Leu	Lys	Tyr	His	Val	Val	Lys	Thr	Pro	Arg	Ser	Val	Tyr	Lys	Thr
			500						505					510		
	Val	Pro	Asp	Cys	Glu	Pro	Cys	Arg	Pro	Leu	Gln	Arg	Ser	Pro	Ile	Glu
		515						520					525			
	Gly	Phe	Tyr	Leu	Ala	Gly	Asp	Tyr	Thr	Lys	Gln	Lys	Tyr	Leu	Ala	Ser
25		530				535						540				
	Met	Glu	Gly	Ala	Val	Leu	Ser	Gly	Lys	Leu	Cys	Ala	Gln	Ala	Ile	Val
	545				550					555						560
	Gln	Asp	Cys	Ser	Leu	Leu	Ala	Ser	Arg	Val	Gln	Lys	Ser	Pro	Gln	Thr
				565					570						575	
30	Leu	Thr	Ile	Ala												
				580												

35 <210> 3  
 <211> 2293  
 <212> DNA  
 <213> Glycine max

40 <220>  
 <221> CDS  
 <222> (221)..(1933)

45 <400> 3  
 gaattccttc tacgtactgc cgtgggtgctt tcaccactgc ttaccactaa ccttcctctc  
 60

tctctctgcc gctgcaagct tgggtactctc aactcaattc tccaccttat tcttttact  
 120

50 tcttcagctc ttgttttttc ccaaactctac tttcaaagtg cctgaattct gcaacagtaa  
 180

55 tattaacact cctctctttt gttcaggctt tatttcccca atg gcc gct tgt ggc  
 235

Met Ala Ala Cys Gly

tat ata tct gct gcc aac ttc aat tat ctc gtt ggc gcc aga aac ata  
 283  
 5 Tyr Ile Ser Ala Ala Asn Phe Asn Tyr Leu Val Gly Ala Arg Asn Ile  
                     10                    15                    20

tcc aaa ttc gct tct tca gac gcc aca att tcg ttt tca ttt ggc ggg  
 331  
 10 Ser Lys Phe Ala Ser Ser Asp Ala Thr Ile Ser Phe Ser Phe Gly Gly  
                     25                    30                    35

agc gac tca atg ggt ctt act ttg cga ccc gct ccg att cgt gct cct  
 379  
 15 Ser Asp Ser Met Gly Leu Thr Leu Arg Pro Ala Pro Ile Arg Ala Pro  
                     40                    45                    50

aag agg aac cat ttc tct ccc ttg cgt gtc gtt tgc gtc gat tat cca  
 427  
 20 Lys Arg Asn His Phe Ser Pro Leu Arg Val Val Cys Val Asp Tyr Pro  
                     55                    60                    65

cgc cca gag ctc gaa aac acc gtt aat ttc gtt gaa gct gct tac ttg  
 475  
 25 Arg Pro Glu Leu Glu Asn Thr Val Asn Phe Val Glu Ala Ala Tyr Leu  
                     70                    75                    80                    85

tct tcc acc ttt cgt gct tct ccg cgt cct cta aaa ccc ttg aac atc  
 523  
 30 Ser Ser Thr Phe Arg Ala Ser Pro Arg Pro Leu Lys Pro Leu Asn Ile  
                     90                    95                    100

gtt att gcc ggt gca gga ttg gct ggt tta tca act gca aaa tat ttg  
 571  
 35 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu  
                     105                    110                    115

gct gat gct ggg cat aaa cct ata ttg ctg gaa gca aga gac gtt cta  
 619  
 40 Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val Leu  
                     120                    125                    130

ggt gga aag gtt gct gcatggg aaa gac aag gat gga gac tgg tac gag  
 667  
 45 Gly Gly Lys Val Ala Ala Trp Lys Asp Lys Asp Gly Asp Trp Tyr Glu  
                     135                    140                    145

aca ggc cta cac atc ttt ttt ggg gct tac cct tat gtg cag aac ctt  
 715  
 50 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Tyr Val Gln Asn Leu  
                     150                    155                    160                    165

ttt gga gaa ctt ggc att aat gat cgg tta caa tgg aaa gag cat tct  
 763  
 55 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser  
                     170                    175                    180

atg att ttt gct atg cca aat aag cct gga gag ttt agt cga ttt gat  
 811  
 5 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp  
 185 190 195

ttt cct gaa gtt ctt ccc tcc cca ttg aat gga ata tgg gca ata ttg  
 859  
 10 Phe Pro Glu Val Leu Pro Ser Pro Leu Asn Gly Ile Trp Ala Ile Leu  
 200 205 210

agg aac aat gag atg ctt aca tgg cca gag aaa gta aaa ttt gca att  
 907  
 15 Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala Ile  
 215 220 225

ggg ctt ctc cca gct atg ctt ggc gga cag cca tat gtt gag gct caa  
 955  
 20 Gly Leu Leu Pro Ala Met Leu Gly Gly Gln Pro Tyr Val Glu Ala Gln  
 230 235 240 245

gat ggt ctt tct gtt caa gaa tgg atg aaa aag cag ggc gta cct gaa  
 1003  
 25 Asp Gly Leu Ser Val Gln Glu Trp Met Lys Lys Gln Gly Val Pro Glu  
 250 255 260

cgg gta gct gat gag gtg ttc ata gca atg tca aag gca cta aac ttc  
 1051  
 30 Arg Val Ala Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe  
 265 270 275

atc aat cct gat gaa ctt tca atg caa tgt ata ttg att gct tta aac  
 1099  
 35 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn  
 280 285 290

cga ttt ctt cag gag aaa cat ggt tct aag atg gcc ttt ttg gat ggc  
 1147  
 40 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly  
 295 300 305

aat cca ccc gaa aga ctt tgt atg cca ata gtt gat tat att cag tcc  
 1195  
 45 Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp Tyr Ile Gln Ser  
 310 315 320 325

ttg ggt ggt gaa gtt cat cta aat tcg cgc att caa aaa att gag cta  
 1243  
 50 Leu Gly Gly Glu Val His Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu  
 330 335 340

aat gat gat gga acg gtg aag agc ttc tta cta aat aat ggg aaa gtg  
 1291  
 55 Asn Asp Asp Gly Thr Val Lys Ser Phe Leu Leu Asn Asn Gly Lys Val  
 345 350 355

atg gaa ggg gat gct tat gtg ttt gca act cca gtg gat att ctg aag  
 1339  
 5 Met Glu Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys  
 360 365 370

ctt ctt cta cca gat aac tgg aaa ggg att cca tat ttc cag aga ttg  
 1387  
 10 Leu Leu Leu Pro Asp Asn Trp Lys Gly Ile Pro Tyr Phe Gln Arg Leu  
 375 380 385

gat aaa tta gtt ggc gtc cca gtc ata aat gtt cac ata tgg ttt gac  
 1435  
 15 Asp Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp  
 390 395 400 405

aga aaa ctg aag aac aca tat gat cac ctt ctc ttt agc aga agt ccc  
 1483  
 20 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro  
 410 415 420

ctt ctg agt gta tat gct gac atg tca gta act tgc aag gaa tat tat  
 1531  
 25 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr  
 425 430 435

agc cca aac cag tca atg tta gag ttg gtt ttt gca cca gcc gaa gaa  
 1579  
 30 Ser Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Glu  
 440 445 450

tgg att tca cgt agt gat gat gat att att caa gcc acg atg act gag  
 1627  
 35 Trp Ile Ser Arg Ser Asp Asp Asp Ile Ile Gln Ala Thr Met Thr Glu  
 455 460 465

ctt gcc aaa ctc ttt cct gat gaa att tct gca gac caa agc aaa gca  
 1675  
 40 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala  
 470 475 480 485

aag att ctc aag tac cat gtt gtt aaa aca cca agg tcg gtt tac aaa  
 1723  
 45 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys  
 490 495 500

act gtt cca aat tgt gaa cct tgt cga ccc att caa aga tct cct ata  
 1771  
 50 Thr Val Pro Asn Cys Glu Pro Cys Arg Pro Ile Gln Arg Ser Pro Ile  
 505 510 515

gaa ggt ttc tat tta gct gga gat tac aca aaa caa aaa tat tta gct  
 1819  
 55 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala  
 520 525 530

tca atg gaa ggc gct gtt ctt tct ggg aag ctt tgt gca cag gct att  
1867  
5 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile  
535 540 545

gta cag gat tct gag cta cta gct act cgg ggc cag aaa aga atg gct  
1915  
10 Val Gln Asp Ser Glu Leu Leu Ala Thr Arg Gly Gln Lys Arg Met Ala  
550 555 560 565

aaa gca agt gtt gtg taa caaaaacaag aattgaaaga gtcattgtag  
1963  
15 Lys Ala Ser Val Val  
570

agtacaggag catcatttca actttggcat tctttgtctg tggtcaggac tcaggagacc  
2023  
20 ttcaacttta ttagttcata cgaataaaga aaggctcagc ttctgaaatt tagctgcacc  
2083

gtcgtcaact gtgtgcaata agctatacgg aacaaacgac atgtgtcaac tttaagtcag  
2143  
25 cccattgttt tgttatcctc caattttctg gatcaatgtt tgtattggaa agaaatatgt  
2203

cattattcaa acttgtttat atccactttt tttatttatc aacatttgtc acaacctttc  
2263  
30 gttgagtaaa aaaaaaaaaa aaaagaattc  
2293

35 <210> 4  
<211> 570  
<212> PRT  
<213> Glycine max

40 <400> 4  
Met Ala Ala Cys Gly Tyr Ile Ser Ala Ala Asn Phe Asn Tyr Leu Val  
1 5 10 15  
45 Gly Ala Arg Asn Ile Ser Lys Phe Ala Ser Ser Asp Ala Thr Ile Ser  
20 25 30  
Phe Ser Phe Gly Gly Ser Asp Ser Met Gly Leu Thr Leu Arg Pro Ala  
35 40 45  
Pro Ile Arg Ala Pro Lys Arg Asn His Phe Ser Pro Leu Arg Val Val  
50 55 60  
50 Cys Val Asp Tyr Pro Arg Pro Glu Leu Glu Asn Thr Val Asn Phe Val  
65 70 75 80  
Glu Ala Ala Tyr Leu Ser Ser Thr Phe Arg Ala Ser Pro Arg Pro Leu  
85 90 95  
55 Lys Pro Leu Asn Ile Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser  
100 105 110  
Thr Ala Lys Tyr Leu Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu  
115 120 125

	Ala	Arg	Asp	Val	Leu	Gly	Gly	Lys	Val	Ala	Ala	Trp	Lys	Asp	Lys	Asp
	130					135						140				
	Gly	Asp	Trp	Tyr	Glu	Thr	Gly	Leu	His	Ile	Phe	Phe	Gly	Ala	Tyr	Pro
	145				150						155					160
5	Tyr	Val	Gln	Asn	Leu	Phe	Gly	Glu	Leu	Gly	Ile	Asn	Asp	Arg	Leu	Gln
				165						170					175	
	Trp	Lys	Glu	His	Ser	Met	Ile	Phe	Ala	Met	Pro	Asn	Lys	Pro	Gly	Glu
				180					185					190		
10	Phe	Ser	Arg	Phe	Asp	Phe	Pro	Glu	Val	Leu	Pro	Ser	Pro	Leu	Asn	Gly
			195				200						205			
	Ile	Trp	Ala	Ile	Leu	Arg	Asn	Asn	Glu	Met	Leu	Thr	Trp	Pro	Glu	Lys
	210					215						220				
	Val	Lys	Phe	Ala	Ile	Gly	Leu	Leu	Pro	Ala	Met	Leu	Gly	Gly	Gln	Pro
	225				230						235					240
15	Tyr	Val	Glu	Ala	Gln	Asp	Gly	Leu	Ser	Val	Gln	Glu	Trp	Met	Lys	Lys
					245					250					255	
	Gln	Gly	Val	Pro	Glu	Arg	Val	Ala	Asp	Glu	Val	Phe	Ile	Ala	Met	Ser
				260					265					270		
20	Lys	Ala	Leu	Asn	Phe	Ile	Asn	Pro	Asp	Glu	Leu	Ser	Met	Gln	Cys	Ile
			275					280						285		
	Leu	Ile	Ala	Leu	Asn	Arg	Phe	Leu	Gln	Glu	Lys	His	Gly	Ser	Lys	Met
	290					295						300				
	Ala	Phe	Leu	Asp	Gly	Asn	Pro	Pro	Glu	Arg	Leu	Cys	Met	Pro	Ile	Val
	305				310						315					320
25	Asp	Tyr	Ile	Gln	Ser	Leu	Gly	Gly	Glu	Val	His	Leu	Asn	Ser	Arg	Ile
				325						330					335	
	Gln	Lys	Ile	Glu	Leu	Asn	Asp	Asp	Gly	Thr	Val	Lys	Ser	Phe	Leu	Leu
				340					345					350		
30	Asn	Asn	Gly	Lys	Val	Met	Glu	Gly	Asp	Ala	Tyr	Val	Phe	Ala	Thr	Pro
			355					360					365			
	Val	Asp	Ile	Leu	Lys	Leu	Leu	Leu	Pro	Asp	Asn	Trp	Lys	Gly	Ile	Pro
	370					375						380				
	Tyr	Phe	Gln	Arg	Leu	Asp	Lys	Leu	Val	Gly	Val	Pro	Val	Ile	Asn	Val
	385				390						395					400
35	His	Ile	Trp	Phe	Asp	Arg	Lys	Leu	Lys	Asn	Thr	Tyr	Asp	His	Leu	Leu
				405						410					415	
	Phe	Ser	Arg	Ser	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Asp	Met	Ser	Val	Thr
				420					425					430		
40	Cys	Lys	Glu	Tyr	Tyr	Ser	Pro	Asn	Gln	Ser	Met	Leu	Glu	Leu	Val	Phe
			435					440					445			
	Ala	Pro	Ala	Glu	Glu	Trp	Ile	Ser	Arg	Ser	Asp	Asp	Asp	Ile	Ile	Gln
	450					455						460				
	Ala	Thr	Met	Thr	Glu	Leu	Ala	Lys	Leu	Phe	Pro	Asp	Glu	Ile	Ser	Ala
	465				470						475					480
45	Asp	Gln	Ser	Lys	Ala	Lys	Ile	Leu	Lys	Tyr	His	Val	Val	Lys	Thr	Pro
				485						490					495	
	Arg	Ser	Val	Tyr	Lys	Thr	Val	Pro	Asn	Cys	Glu	Pro	Cys	Arg	Pro	Ile
				500					505					510		
50	Gln	Arg	Ser	Pro	Ile	Glu	Gly	Phe	Tyr	Leu	Ala	Gly	Asp	Tyr	Thr	Lys
			515					520					525			
	Gln	Lys	Tyr	Leu	Ala	Ser	Met	Glu	Gly	Ala	Val	Leu	Ser	Gly	Lys	Leu
			530				535					540				
	Cys	Ala	Gln	Ala	Ile	Val	Gln	Asp	Ser	Glu	Leu	Leu	Ala	Thr	Arg	Gly
	545				550						555					560
55	Gln	Lys	Arg	Met	Ala	Lys	Ala	Ser	Val	Val						
				565						570						

<210> 5  
 <211> 2264  
 5 <212> DNA  
 <213> Zea mays  
  
 <220>  
 <221> CDS  
 10 <222> (351)..(2066)  
  
 <400> 5  
 ctccaaatgc ggaggtctcg actcttctct cttcctccat ctttatcatc gccccacgta  
 60  
 15 cacacccaat tctctgcaac tgggctcccc cgcctccacg acactgcccc ccgtctcaag  
 120  
 tccgccgcct ccattcttca gctctcctat cctccgccta gaatatcttc atcggtattt  
 20 180  
 taccaacctg gatcaattta ctcacgatac tctgaagcgt atacatatgc catatgggaa  
 240  
 25 atgacttcat agctgtgggt tgtcttatgg ctccttgaat ttgcagtagt ctgcctgtac  
 300  
 ctattggctg aagcagagct gacccccact ttatcaagag ttgctcaacg atg gac  
 356  
 30 Met Asp  
 1  
  
 act ggc tgc ctg tca tct atg aat att act gga gct agc cag aca aga  
 404  
 35 Thr Gly Cys Leu Ser Ser Met Asn Ile Thr Gly Ala Ser Gln Thr Arg  
 5 10 15  
  
 tct ttt gcg ggg caa ctt cct cct cag aga tgt ttt gcg agt agt cac  
 452  
 40 Ser Phe Ala Gly Gln Leu Pro Pro Gln Arg Cys Phe Ala Ser Ser His  
 20 25 30  
  
 tat aca agc ttt gcc gtg aaa aaa ctt gtc tca agg aat aaa gga agg  
 500  
 45 Tyr Thr Ser Phe Ala Val Lys Lys Leu Val Ser Arg Asn Lys Gly Arg  
 35 40 45 50  
  
 aga tca cac cgt aga cat cct gcc ttg cag gtt gtc tgc aag gat ttt  
 548  
 50 Arg Ser His Arg Arg His Pro Ala Leu Gln Val Val Cys Lys Asp Phe  
 55 60 65  
  
 cca aga cct cca cta gaa agc aca ata aac tat ttg gaa gct gga cag  
 596  
 55 Pro Arg Pro Pro Leu Glu Ser Thr Ile Asn Tyr Leu Glu Ala Gly Gln

	70	75	80
	ctc tct tca ttt ttt aga aac agc gaa cgc ccc agt aag ccg ttg cag		
	644		
5	Leu Ser Ser Phe Phe Arg Asn Ser Glu Arg Pro Ser Lys Pro Leu Gln	90	95
	85		
	gtc gtg gtt gct ggt gca gga ttg gct ggt cta tca aca gcg aag tat		
	692		
10	Val Val Val Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr	105	110
	100		
	ctg gca gat gct ggc cat aaa ccc ata ttg ctt gag gca aga gat gtt		
	740		
15	Leu Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val	120	125
	115		130
	ttg ggt gga aag gta gct gct tgg aag gat gaa gat gga gat tgg tac		
	788		
20	Leu Gly Gly Lys Val Ala Ala Trp Lys Asp Glu Asp Gly Asp Trp Tyr	135	140
			145
	gag act ggg ctt cat ata ttt ttt gga gct tat ccc aac ata cag aat		
	836		
25	Glu Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Ile Gln Asn	150	155
			160
	ctg ttt ggc gag ctt agg att gag gat cgt ttg cag tgg aaa gaa cac		
	884		
30	Leu Phe Gly Glu Leu Arg Ile Glu Asp Arg Leu Gln Trp Lys Glu His	165	170
			175
	tct atg ata ttc gcc atg cca aac aag cca gga gaa ttc agc cgg ttc		
	932		
35	Ser Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe	180	185
			190
	gat ttc cca gaa act ttg cca gca cct ata aat ggg ata tgg gcc ata		
	980		
40	Asp Phe Pro Glu Thr Leu Pro Ala Pro Ile Asn Gly Ile Trp Ala Ile	195	200
			205
	ttg aga aac aat gaa atg ctt act tgg ccg gag aag gtg aag ttt gca		
	1028		
45	Leu Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala	215	220
			225
	atc gga ctt ctg cca gca atg gtt ggt ggt caa cct tat gtt gaa gct		
	1076		
50	Ile Gly Leu Leu Pro Ala Met Val Gly Gly Gln Pro Tyr Val Glu Ala	230	235
			240
	caa gat ggc tta acc gtt tca gaa tgg atg aaa aag cag ggt gtt cct		
	1124		
55	Gln Asp Gly Leu Thr Val Ser Glu Trp Met Lys Lys Gln Gly Val Pro	245	250
			255

gat cgg gtg aac gat gag gtt ttt att gca atg tcc aag gca ctc aat  
 1172  
 5 Asp Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn  
 260 265 270

ttc ata aat cct gat gag cta tct atg cag tgc att ttg att gct ttg  
 1220  
 10 Phe Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu  
 275 280 285 290

aac cga ttt ctt cag gag aag cat ggt tct aaa atg gca ttc ttg gat  
 1268  
 15 Asn Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp  
 295 300 305

ggt aat ccg cct gaa agg cta tgc atg cct att gtt gat cac att cgg  
 1316  
 20 Gly Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp His Ile Arg  
 310 315 320

tct agg ggt gga gag gtc cgc ctg aat tct cgt att aaa aag ata gag  
 1364  
 25 Ser Arg Gly Gly Glu Val Arg Leu Asn Ser Arg Ile Lys Lys Ile Glu  
 325 330 335

ctg aat cct gat gga act gta aaa cac ttc gca ctt agt gat gga act  
 1412  
 30 Leu Asn Pro Asp Gly Thr Val Lys His Phe Ala Leu Ser Asp Gly Thr  
 340 345 350

caa ata act gga gat gct tat gtt tgt gca aca cca gtc gat atc ttc  
 1460  
 35 Gln Ile Thr Gly Asp Ala Tyr Val Cys Ala Thr Pro Val Asp Ile Phe  
 355 360 365 370

aag ctt ctt gta cct caa gag tgg agt gaa att act tat ttc aag aaa  
 1508  
 40 Lys Leu Leu Val Pro Gln Glu Trp Ser Glu Ile Thr Tyr Phe Lys Lys  
 375 380 385

ctg gag aag ttg gtg gga gtt cct gtt atc aat gtt cat ata tgg ttt  
 1556  
 45 Leu Glu Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe  
 390 395 400

gac aga aaa ctg aac aac aca tat gac cac ctt ctt ttc agc agg agt  
 1604  
 50 Asp Arg Lys Leu Asn Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser  
 405 410 415

tca ctt tta agt gtc tat gca gac atg tca gta acc tgc aag gaa tac  
 1652  
 55 Ser Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr  
 420 425 430

tat gac cca aac cgt tca atg ctg gag ttg gtc ttt gct cct gca gac  
 1700  
 Tyr Asp Pro Asn Arg Ser Met Leu Glu Leu Val Phe Ala Pro Ala Asp  
 5 435 440 445 450  
 gaa tgg att ggt cga agt gac act gaa atc atc gat gca act atg gaa  
 1748  
 Glu Trp Ile Gly Arg Ser Asp Thr Glu Ile Ile Asp Ala Thr Met Glu  
 10 455 460 465  
 gag cta gcc aag tta ttt cct gat gaa att gct gct gat cag agt aaa  
 1796  
 Glu Leu Ala Lys Leu Phe Pro Asp Glu Ile Ala Ala Asp Gln Ser Lys  
 15 470 475 480  
 gca aag att ctt aag tat cat att gtg aag aca ccg aga tcg gtt tac  
 1844  
 Ala Lys Ile Leu Lys Tyr His Ile Val Lys Thr Pro Arg Ser Val Tyr  
 20 485 490 495  
 aaa act gtc cca aac tgt gag cct tgc cgg cct ctc caa agg tca cct  
 1892  
 Lys Thr Val Pro Asn Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro  
 25 500 505 510  
 atc gaa ggt ttc tat cta gct ggt gat tac aca aag cag aaa tac ctg  
 1940  
 Ile Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu  
 30 515 520 525 530  
 gct tct atg gaa ggt gca gtc cta tcc ggg aag ctt tgt gcc cag tcc  
 1988  
 Ala Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ser  
 35 535 540 545  
 ata gtg cag gat tat agc agg ctc gca ctc agg agc cag aaa agc cta  
 2036  
 Ile Val Gln Asp Tyr Ser Arg Leu Ala Leu Arg Ser Gln Lys Ser Leu  
 40 550 555 560  
 caa tca gga gaa gtt ccc gtc cca tct tag ttgtagttgg ctttagctat  
 2086  
 Gln Ser Gly Glu Val Pro Val Pro Ser  
 45 565 570  
 cgtcaccccc actgggtgct atcttatctc ctatttcaat gggaaccac ccaatgggtca  
 2146  
 50 tgttgagagac aacacctgtt atggctcttt gaccatctcg tggtgactgt agttgatgtc  
 2206  
 atattcggat atatatgtaa aaggacctgc atagcaattg ttagaccttg gaaaaaaa  
 2264  
 55  
 <210> 6

<211> 571  
 <212> PRT  
 <213> Zea mays

5 <400> 6  
 Met Asp Thr Gly Cys Leu Ser Ser Met Asn Ile Thr Gly Ala Ser Gln  
 1 5 10 15  
 Thr Arg Ser Phe Ala Gly Gln Leu Pro Pro Gln Arg Cys Phe Ala Ser  
 20 25 30  
 10 Ser His Tyr Thr Ser Phe Ala Val Lys Lys Leu Val Ser Arg Asn Lys  
 35 40 45  
 Gly Arg Arg Ser His Arg Arg His Pro Ala Leu Gln Val Val Cys Lys  
 50 55 60  
 15 Asp Phe Pro Arg Pro Pro Leu Glu Ser Thr Ile Asn Tyr Leu Glu Ala  
 65 70 75 80  
 Gly Gln Leu Ser Ser Phe Phe Arg Asn Ser Glu Arg Pro Ser Lys Pro  
 85 90 95  
 Leu Gln Val Val Val Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala  
 100 105 110  
 20 Lys Tyr Leu Ala Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg  
 115 120 125  
 Asp Val Leu Gly Gly Lys Val Ala Ala Trp Lys Asp Glu Asp Gly Asp  
 130 135 140  
 25 Trp Tyr Glu Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Ile  
 145 150 155 160  
 Gln Asn Leu Phe Gly Glu Leu Arg Ile Glu Asp Arg Leu Gln Trp Lys  
 165 170 175  
 Glu His Ser Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser  
 180 185 190  
 30 Arg Phe Asp Phe Pro Glu Thr Leu Pro Ala Pro Ile Asn Gly Ile Trp  
 195 200 205  
 Ala Ile Leu Arg Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys  
 210 215 220  
 Phe Ala Ile Gly Leu Leu Pro Ala Met Val Gly Gly Gln Pro Tyr Val  
 225 230 235 240  
 35 Glu Ala Gln Asp Gly Leu Thr Val Ser Glu Trp Met Lys Lys Gln Gly  
 245 250 255  
 Val Pro Asp Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala  
 260 265 270  
 40 Leu Asn Phe Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile  
 275 280 285  
 Ala Leu Asn Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe  
 290 295 300  
 Leu Asp Gly Asn Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp His  
 305 310 315 320  
 45 Ile Arg Ser Arg Gly Gly Glu Val Arg Leu Asn Ser Arg Ile Lys Lys  
 325 330 335  
 Ile Glu Leu Asn Pro Asp Gly Thr Val Lys His Phe Ala Leu Ser Asp  
 340 345 350  
 50 Gly Thr Gln Ile Thr Gly Asp Ala Tyr Val Cys Ala Thr Pro Val Asp  
 355 360 365  
 Ile Phe Lys Leu Leu Val Pro Gln Glu Trp Ser Glu Ile Thr Tyr Phe  
 370 375 380  
 Lys Lys Leu Glu Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile  
 385 390 395 400  
 55 Trp Phe Asp Arg Lys Leu Asn Asn Thr Tyr Asp His Leu Leu Phe Ser

405 410 415  
 Arg Ser Ser Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys  
 420 425 430  
 5 Glu Tyr Tyr Asp Pro Asn Arg Ser Met Leu Glu Leu Val Phe Ala Pro  
 435 440 445  
 Ala Asp Glu Trp Ile Gly Arg Ser Asp Thr Glu Ile Ile Asp Ala Thr  
 450 455 460  
 Met Glu Glu Leu Ala Lys Leu Phe Pro Asp Glu Ile Ala Ala Asp Gln  
 465 470 475 480  
 10 Ser Lys Ala Lys Ile Leu Lys Tyr His Ile Val Lys Thr Pro Arg Ser  
 485 490 495  
 Val Tyr Lys Thr Val Pro Asn Cys Glu Pro Cys Arg Pro Leu Gln Arg  
 500 505 510  
 15 Ser Pro Ile Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys  
 515 520 525  
 Tyr Leu Ala Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala  
 530 535 540  
 Gln Ser Ile Val Gln Asp Tyr Ser Arg Leu Ala Leu Arg Ser Gln Lys  
 545 550 555 560  
 20 Ser Leu Gln Ser Gly Glu Val Pro Val Pro Ser  
 565 570

25 <210> 7  
 <211> 2027  
 <212> DNA  
 <213> Oryza sativa

30 <220>  
 <221> CDS  
 <222> (5)..(1705)

<400> 7  
 35 gttt atg aca gca tct gcc aga tat ttt gca gga caa ctt cct act cat  
 49  
 Met Thr Ala Ser Ala Arg Tyr Phe Ala Gly Gln Leu Pro Thr His  
 1 5 10 15

40 agg tgc ttc gca agt agc agc atc caa gca ctg aaa ggt agt cag cat  
 97  
 Arg Cys Phe Ala Ser Ser Ser Ile Gln Ala Leu Lys Gly Ser Gln His  
 20 25 30

45 gtg agc ttt gga gtg aaa tct ctt gtc tta agg aat aaa gga aaa aga  
 145  
 Val Ser Phe Gly Val Lys Ser Leu Val Leu Arg Asn Lys Gly Lys Arg  
 35 40 45

50 ttc cgt cgg agg ctc ggt gct cta cag gtt gtt tgc cag gac ttt cca  
 193  
 Phe Arg Arg Arg Leu Gly Ala Leu Gln Val Val Cys Gln Asp Phe Pro  
 50 55 60

55 aga cct cca cta gaa aac aca ata aac ttt ttg gaa gct gga caa cta  
 241

	Arg	Pro	Pro	Leu	Glu	Asn	Thr	Ile	Asn	Phe	Leu	Glu	Ala	Gly	Gln	Leu
		65					70					75				
5	tcc	tca	ttt	ttc	aga	aac	agt	gaa	caa	ccc	act	aaa	cca	tta	cag	gtc
	289															
	Ser	Ser	Phe	Phe	Arg	Asn	Ser	Glu	Gln	Pro	Thr	Lys	Pro	Leu	Gln	Val
	80					85					90					95
10	gtg	att	gct	gga	gca	gga	tta	gct	ggt	tta	tca	acg	gca	aaa	tat	ctg
	337															
	Val	Ile	Ala	Gly	Ala	Gly	Leu	Ala	Gly	Leu	Ser	Thr	Ala	Lys	Tyr	Leu
					100					105					110	
15	gca	gat	gct	ggt	cat	aaa	ccc	ata	ttg	ctt	gag	gca	agg	gat	gtt	ttg
	385															
	Ala	Asp	Ala	Gly	His	Lys	Pro	Ile	Leu	Leu	Glu	Ala	Arg	Asp	Val	Leu
				115					120					125		
20	ggt	gga	aag	ata	gct	gct	tgg	aag	gat	gaa	gat	gga	gat	tgg	tat	gaa
	433															
	Gly	Gly	Lys	Ile	Ala	Ala	Trp	Lys	Asp	Glu	Asp	Gly	Asp	Trp	Tyr	Glu
			130					135					140			
25	act	ggg	ctt	cat	atc	ttt	ttt	gga	gct	tat	ccc	aac	ata	cag	aac	ttg
	481															
	Thr	Gly	Leu	His	Ile	Phe	Phe	Gly	Ala	Tyr	Pro	Asn	Ile	Gln	Asn	Leu
		145					150					155				
30	ttt	ggc	gag	ctt	ggt	att	aat	gat	cgg	ttg	caa	tgg	aag	gaa	cac	tcc
	529															
	Phe	Gly	Glu	Leu	Gly	Ile	Asn	Asp	Arg	Leu	Gln	Trp	Lys	Glu	His	Ser
	160					165					170					175
35	atg	ata	ttt	gcc	atg	cca	aac	aag	cca	gga	gaa	tcc	agc	cgg	ttt	gat
	577															
	Met	Ile	Phe	Ala	Met	Pro	Asn	Lys	Pro	Gly	Glu	Ser	Ser	Arg	Phe	Asp
					180					185					190	
40	ttt	cct	gaa	aca	ttg	cct	gca	ccc	tta	aat	gga	ata	tgg	gcc	ata	cta
	625															
	Phe	Pro	Glu	Thr	Leu	Pro	Ala	Pro	Leu	Asn	Gly	Ile	Trp	Ala	Ile	Leu
				195					200					205		
45	aga	aac	aat	gaa	atg	cta	act	tgg	cca	gag	aag	gtg	aag	ttt	gct	ctt
	673															
	Arg	Asn	Asn	Glu	Met	Leu	Thr	Trp	Pro	Glu	Lys	Val	Lys	Phe	Ala	Leu
		210						215					220			
50	gga	ctt	ttg	cca	gca	atg	gtt	ggt	ggc	caa	gct	tat	gtt	gaa	gct	caa
	721															
	Gly	Leu	Leu	Pro	Ala	Met	Val	Gly	Gly	Gln	Ala	Tyr	Val	Glu	Ala	Gln
		225					230					235				
55	gat	ggt	ttt	act	gtt	tct	gag	tgg	atg	aaa	aag	cag	ggt	gtt	cct	gat
	769															
	Asp	Gly	Phe	Thr	Val	Ser	Glu	Trp	Met	Lys	Lys	Gln	Gly	Val	Pro	Asp

	240		245		250		255									
	cga	gtg	aac	gat	gaa	gtt	ttc	att	gca	atg	tca	aag	gca	ctt	aat	ttc
	817															
5	Arg	Val	Asn	Asp	Glu	Val	Phe	Ile	Ala	Met	Ser	Lys	Ala	Leu	Asn	Phe
					260					265					270	
	ata	aat	cct	gat	gag	tta	tcc	atg	cag	tgc	att	ctg	att	gct	tta	aac
	865															
10	Ile	Asn	Pro	Asp	Glu	Leu	Ser	Met	Gln	Cys	Ile	Leu	Ile	Ala	Leu	Asn
				275					280					285		
	cga	ttt	ctt	cag	gag	aag	cat	ggc	tct	aag	atg	gca	ttc	ttg	gat	ggc
	913															
15	Arg	Phe	Leu	Gln	Glu	Lys	His	Gly	Ser	Lys	Met	Ala	Phe	Leu	Asp	Gly
			290					295					300			
	aat	cct	cct	gaa	agg	tta	tgc	atg	cct	att	gtt	gac	cat	gtt	cgc	tct
	961															
20	Asn	Pro	Pro	Glu	Arg	Leu	Cys	Met	Pro	Ile	Val	Asp	His	Val	Arg	Ser
		305					310					315				
	ttg	ggc	ggc	gag	gtt	cgc	ctg	aat	tct	cgt	att	cag	aaa	ata	gaa	ctt
	1009															
25	Leu	Gly	Gly	Glu	Val	Arg	Leu	Asn	Ser	Arg	Ile	Gln	Lys	Ile	Glu	Leu
	320					325					330				335	
	aat	cct	gat	gga	aca	gtg	aaa	cac	ttt	gca	ctt	acc	gat	gga	act	caa
	1057															
30	Asn	Pro	Asp	Gly	Thr	Val	Lys	His	Phe	Ala	Leu	Thr	Asp	Gly	Thr	Gln
					340					345					350	
	ata	act	gga	gat	gct	tat	gtt	ttt	gca	aca	cca	gtt	gat	atc	ttg	aag
	1105															
35	Ile	Thr	Gly	Asp	Ala	Tyr	Val	Phe	Ala	Thr	Pro	Val	Asp	Ile	Leu	Lys
				355					360					365		
	ctt	ctt	gta	cct	caa	gag	tgg	aaa	gaa	ata	tct	tat	ttc	aag	aag	ctg
	1153															
40	Leu	Leu	Val	Pro	Gln	Glu	Trp	Lys	Glu	Ile	Ser	Tyr	Phe	Lys	Lys	Leu
			370					375					380			
	gag	aag	ttg	gtg	gga	gtt	cct	gtt	ata	aat	gtt	cat	ata	tgg	ttt	gat
	1201															
45	Glu	Lys	Leu	Val	Gly	Val	Pro	Val	Ile	Asn	Val	His	Ile	Trp	Phe	Asp
		385					390					395				
	aga	aaa	ctg	aag	aac	aca	tat	gac	cac	ctt	ctt	ttc	agc	agg	agt	tca
	1249															
50	Arg	Lys	Leu	Lys	Asn	Thr	Tyr	Asp	His	Leu	Leu	Phe	Ser	Arg	Ser	Ser
	400					405					410					415
	ctt	tta	agt	gtt	tat	gcg	gac	atg	tca	gta	act	tgc	aag	gaa	tac	tat
	1297															
55	Leu	Leu	Ser	Val	Tyr	Ala	Asp	Met	Ser	Val	Thr	Cys	Lys	Glu	Tyr	Tyr
					420					425					430	

gat cca agc cgt tca atg ctg gag ttg gtc ttt gct cct gca gag gaa  
 1345  
 5 Asp Pro Ser Arg Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Glu  
 435 440 445

tgg gtt gga cgg agt gac act gaa atc atc gaa gca act atg caa gag  
 1393  
 10 Trp Val Gly Arg Ser Asp Thr Glu Ile Ile Glu Ala Thr Met Gln Glu  
 450 455 460

cta gcc aag cta ttt cct gat gaa att gct gct gat cag agt aaa gca  
 1441  
 15 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ala Ala Asp Gln Ser Lys Ala  
 465 470 475

aag att ctg aag tat cat gtt gtg aag aca cca aga tct gtt tac aag  
 1489  
 20 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys  
 480 485 490 495

act atc ccg gac tgt gaa cct tgc cga cct ctg caa aga tca ccg att  
 1537  
 25 Thr Ile Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile  
 500 505 510

gaa ggg ttc tat cta gct ggt gac tac aca aag cag aaa tat ttg gct  
 1585  
 30 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala  
 515 520 525

tcg atg gag ggt gca gtt cta tct ggg aag ctt tgt gct cag tct gta  
 1633  
 35 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ser Val  
 530 535 540

gtg gag gat tat aaa atg cta tct cgt agg agc ctg aaa agt ctg cag  
 1681  
 40 Val Glu Asp Tyr Lys Met Leu Ser Arg Arg Ser Leu Lys Ser Leu Gln  
 545 550 555

tcc gaa gtt cct gtt gcc tcc tag ttgtagtcag gactattccc aatggtgtgt  
 1735  
 45 Ser Glu Val Pro Val Ala Ser  
 560 565

gtgtcatcat ccctagtca gtttttttct atttagtggg tgcccaactc tccaccaatt  
 1795

50 tacacatgat ggaacttgaa agatgcctat tttggtctta tcatatttct gtaaagttga  
 1855

tttgtgactg agagctgatg ccgatatgcc acgctggaga aaaagaacat tatgtaaaac  
 1915

gacctgcata gtaattctta gactttttgca aaaggcaaaa ggggttaaagc gacctttttt  
1975

5 ttctatgtga agggattaag agaccttaaa aaaaaaaaaa aaaaaaaaaa aa  
2027

10 <210> 8  
<211> 566  
<212> PRT  
<213> Oryza sativa

<400> 8  
15 Met Thr Ala Ser Ala Arg Tyr Phe Ala Gly Gln Leu Pro Thr His Arg  
1 5 10 15  
Cys Phe Ala Ser Ser Ser Ile Gln Ala Leu Lys Gly Ser Gln His Val  
20 20 25 30  
Ser Phe Gly Val Lys Ser Leu Val Leu Arg Asn Lys Gly Lys Arg Phe  
35 40 45  
20 Arg Arg Arg Leu Gly Ala Leu Gln Val Val Cys Gln Asp Phe Pro Arg  
50 55 60  
Pro Pro Leu Glu Asn Thr Ile Asn Phe Leu Glu Ala Gly Gln Leu Ser  
65 70 75 80  
25 Ser Phe Phe Arg Asn Ser Glu Gln Pro Thr Lys Pro Leu Gln Val Val  
85 90 95  
Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu Ala  
100 105 110  
30 Asp Ala Gly His Lys Pro Ile Leu Leu Glu Ala Arg Asp Val Leu Gly  
115 120 125  
Gly Lys Ile Ala Ala Trp Lys Asp Glu Asp Gly Asp Trp Tyr Glu Thr  
130 135 140  
Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Ile Gln Asn Leu Phe  
145 150 155 160  
35 Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser Met  
165 170 175  
Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Ser Ser Arg Phe Asp Phe  
180 185 190  
Pro Glu Thr Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu Arg  
195 200 205  
40 Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Lys Phe Ala Leu Gly  
210 215 220  
Leu Leu Pro Ala Met Val Gly Gly Gln Ala Tyr Val Glu Ala Gln Asp  
225 230 235 240  
45 Gly Phe Thr Val Ser Glu Trp Met Lys Lys Gln Gly Val Pro Asp Arg  
245 250 255  
Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe Ile  
260 265 270  
Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn Arg  
275 280 285  
50 Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly Asn  
290 295 300  
Pro Pro Glu Arg Leu Cys Met Pro Ile Val Asp His Val Arg Ser Leu  
305 310 315 320  
55 Gly Gly Glu Val Arg Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu Asn  
325 330 335  
Pro Asp Gly Thr Val Lys His Phe Ala Leu Thr Asp Gly Thr Gln Ile

[illegible]